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PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSTGTFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLQLQALEAPE
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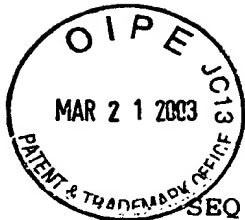
FIG. 1

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CCGTGCCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTC
GCGCACGCTGGTTTTCTGCTTGAGACACGCATCGTGTCCACCTGGTGGCGGCGTGATTGCC
CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCAGGCACCTTCTCAGCC
AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
CTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC
CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAG
GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCCTTGAGCTGAAGCTGCGTCGGCGG
CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGGCGGCTGCTGCAGGCGCTG
CGCGTGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCTGTGCAC
TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCTTGCCTGAAAGAGG
CTTTTTTTTAAATAAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

FIG. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCTCTGNNG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGGCGGCTGATTGCCCCGGGCACCCCCAGCCA
GAACACGCAGTGCTTAGCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
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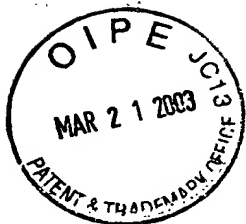
FIG. 3



SEQ ID NO: 4	128	GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
SEQ ID NO: 5	1	GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACG
SEQ ID NO: 6	1	G
SEQ ID NO: 3	1	GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
SEQ ID NO: 4	178	CA-TTCTGGAACCTACCTGGAGCGC
SEQ ID NO: 5	51	CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG
SEQ ID NO: 6	2	CAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
SEQ ID NO: 3	51	CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG
SEQ ID NO: 5	101	GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGCGCCT
SEQ ID NO: 6	52	GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT
SEQ ID NO: 7	1	GAGGGGCCCCCAGGAGTGGTGGCCGGAGGTG
SEQ ID NO: 3	101	GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT
SEQ ID NO: 5	151	GCNGCTGCAGCACCGGNTTCTTCGCGCACGCTGNTTTCTGCTTGAGCAC
SEQ ID NO: 6	102	GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGCAC
SEQ ID NO: 7	32	TGGCAGGGGTGAGGTTGCTGGTCCCAGCCTTGACCCCTGAGCTAGGACAC
SEQ ID NO: 3	151	GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGCAC
SEQ ID NO: 5	201	GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
SEQ ID NO: 6	152	GCATCGTGTCCACCTGGTGCCGGCGTGATTNCCCCGGGCACCCCCAGCCA
SEQ ID NO: 7	82	CAGTTCCCCCTGACCTTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
SEQ ID NO: 8	1	GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
SEQ ID NO: 10	1	CTTGTCCACCTGGTGCCGGCGTGATTNCCC-GGGCACCCCCAGCCA
SEQ ID NO: 3	201	GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
SEQ ID NO: 5	251	GAACACGCA-TGCAAAGCCGTG
SEQ ID NO: 7	132	GAACACGCAGN-CC-AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 8	51	GAACACGCAG-GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 10	47	GAACACGCAGTGCC-AGCCNT-CCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 9	1	AGCNGTGCNCCNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID NO: 3	251	GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 7	182	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 8	101	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 10	97	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGNC-T
SEQ ID NO: 9	36	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 3	301	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 7	232	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAG
SEQ ID NO: 8	151	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO: 10	147	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO: 9	86	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACGCTGTGCACCAGCT
SEQ ID NO: 3	351	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO: 10	197	GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
SEQ ID NO: 9	136	GCACTGGCTTCCCCCTCAGCACCAGGGTANCAGGAGCTGAGGAGTGTGAG
SEQ ID NO: 3	401	GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
SEQ ID NO: 10	247	CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO: 9	186	CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO: 3	451	CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT

FIG. 4

Avi Ashkenazi et al.
U.S.S.N. 09/896,096
DcR3 POLYPEPTIDE, A TNFR HOMOLOG
Sheet 3 of 13



DcR3 1 M R A L E G P G L S L C L V L A L P A L L P V P A V R G V A 31
OPG 1 M N K L L C C A L V F L D L S I K W T T Q E T F P - - - - - 25

DcR3 32 E T P T Y P W R R D A E T G E R L V C A Q C P P G T F V Q R P C 62
OPG 26 - - P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93
OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

DcR3 94 L C G E R E E A R A C H A T H N R A C R C R T G F F A H A G 124
OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155
OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

DcR3 156 G T F S A S S S E Q C Q P H R N C T A L G L A L N V P G S 186
OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217
OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247
OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277
OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300
OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

FIG. 6

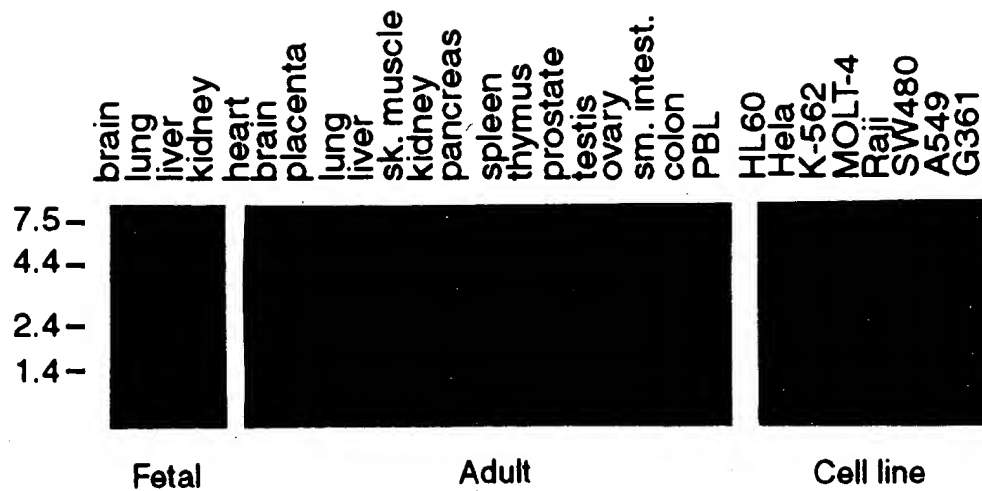


FIG. 7

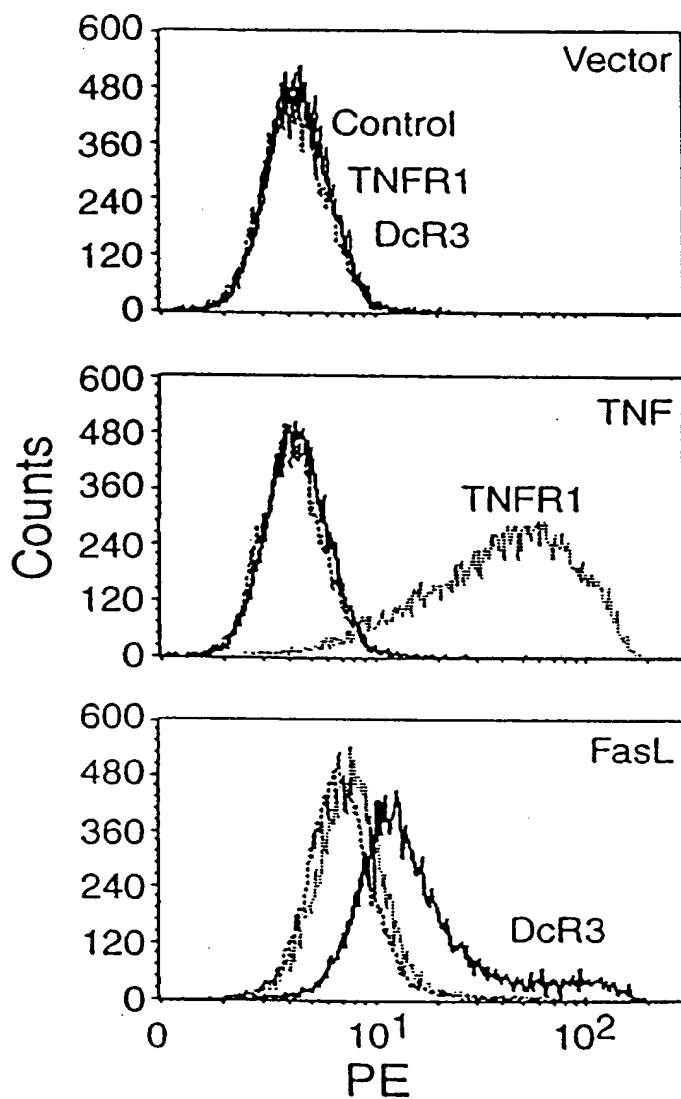


FIG. 8A

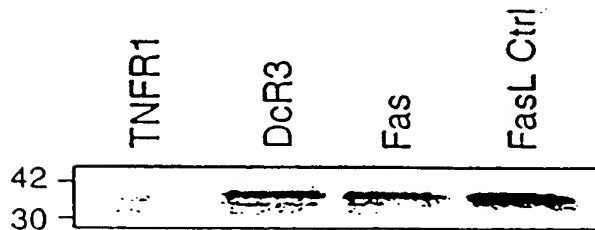


FIG. 8B

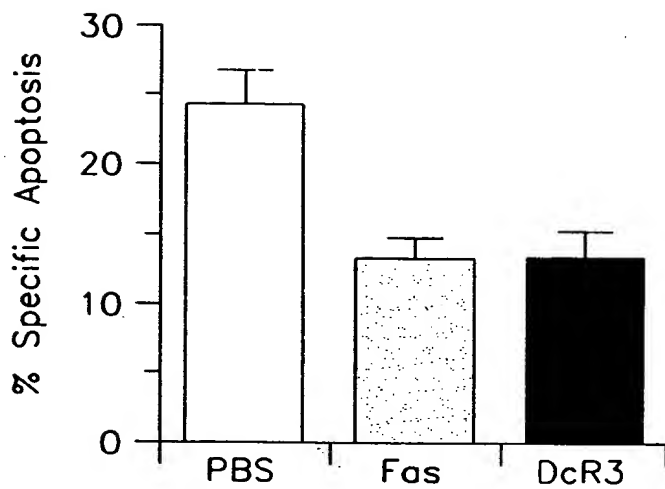


FIG. 9A

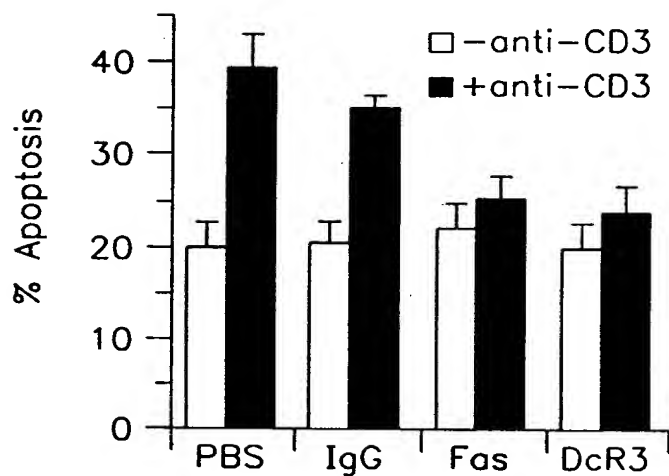


FIG. 9B

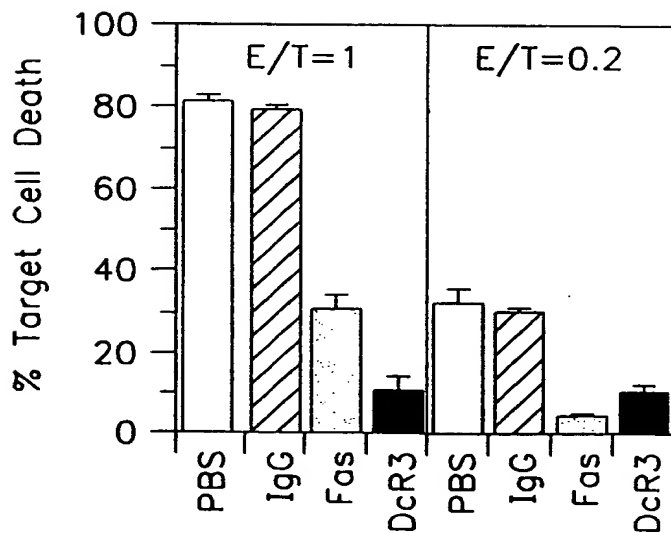


FIG. 9C

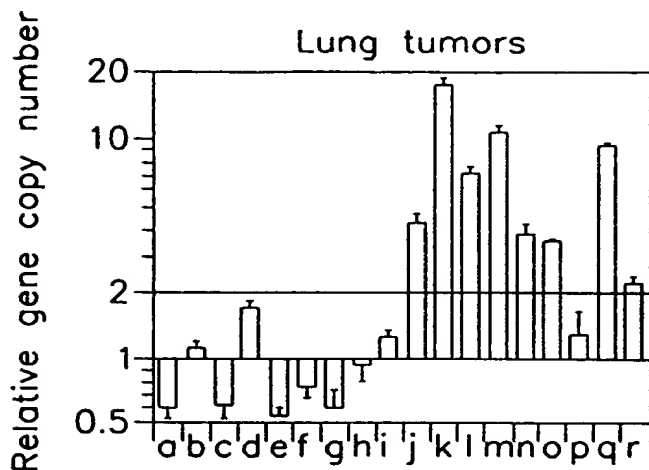
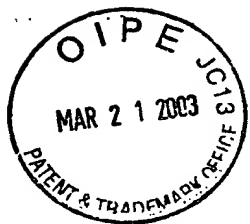


FIG. IOA

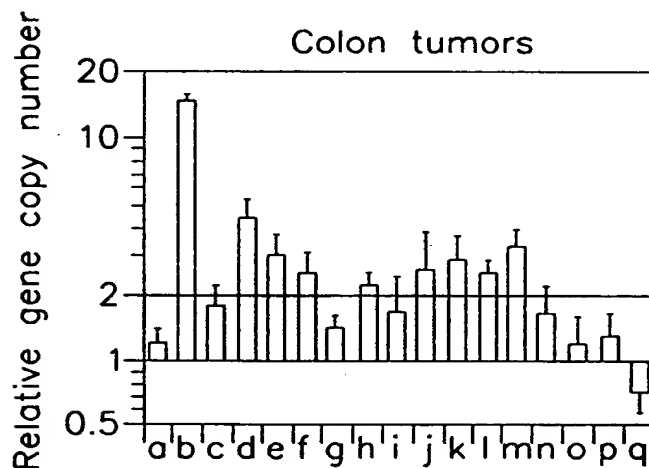


FIG. IOB

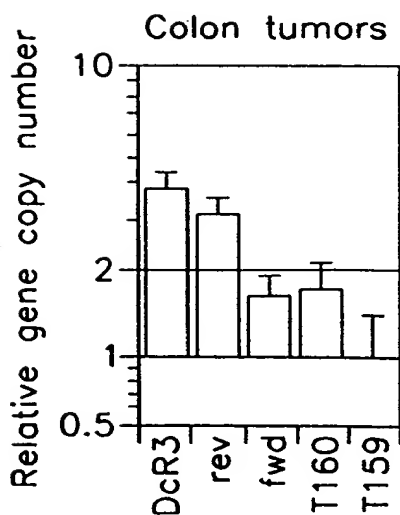


FIG. IOC

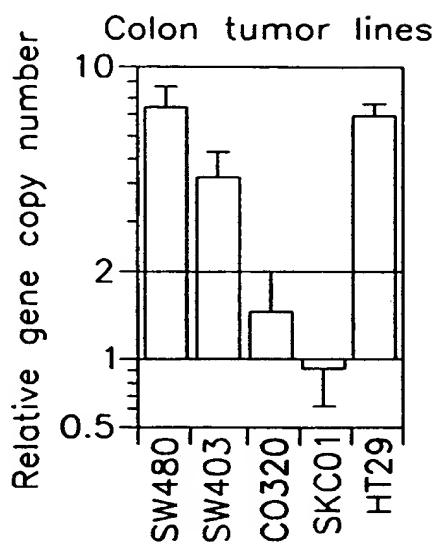


FIG. IOD

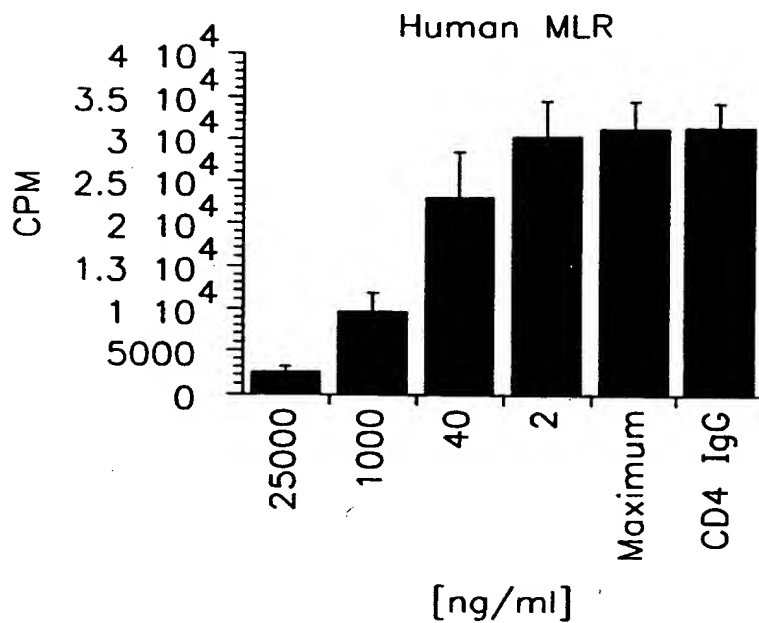


FIG. 1 IA

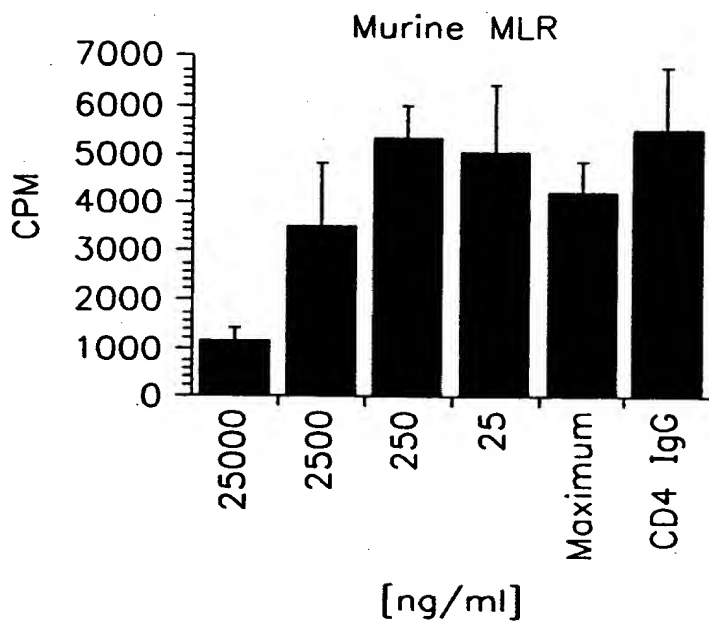


FIG. 1 IB

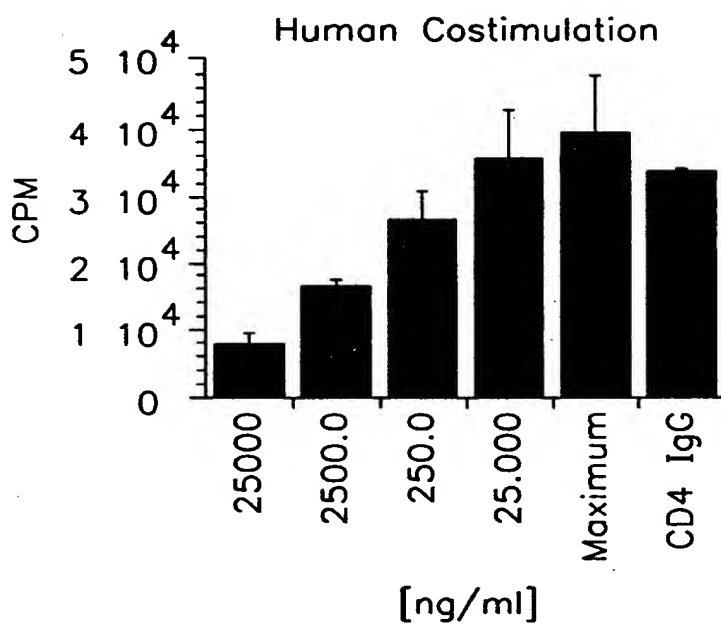


FIG. 1 IC



mAb	Isotype	Antigen Specificity (ELISA)				% Blocking (ELISA)
		DcR3	DR4	DR5	DcR1 OPG	
4B7.1.1	IgG1	+++	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.
% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

FIG. 12

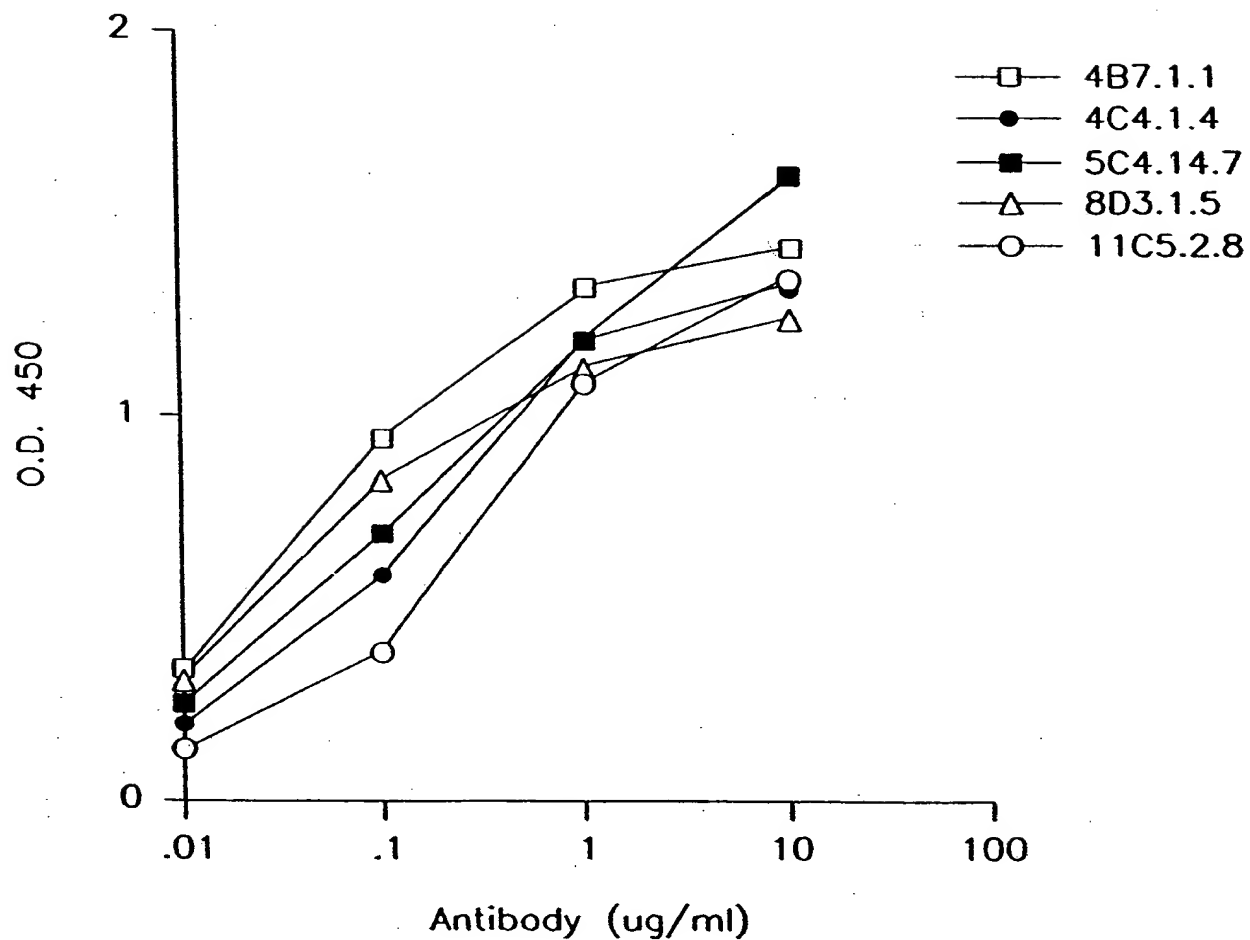


FIG. 13

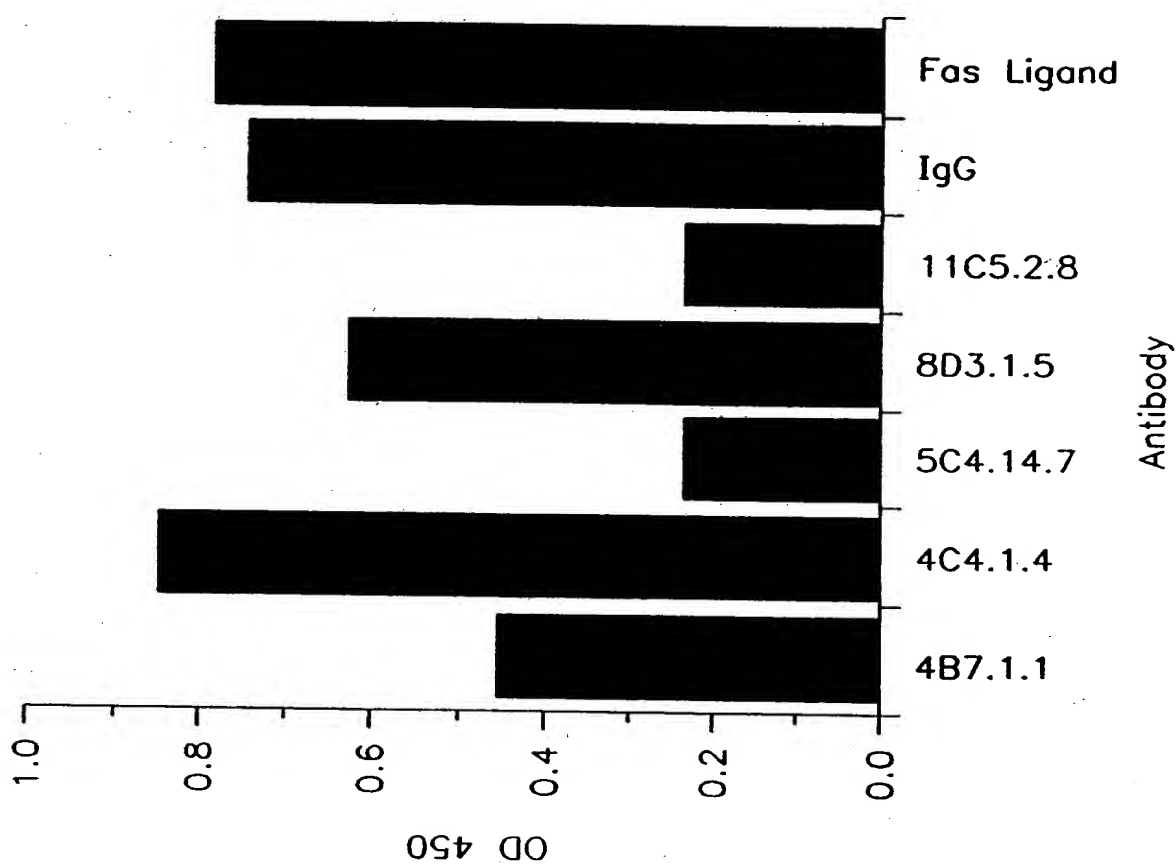


FIG. 14